

SEQUENCE LISTING

(1) GENERAL INFORMATION

- (i) APPLICANT: Bandman, Olga
Au-Young, Janice
Goli, Surya K.
Hillman, Jennifer L.
 - (ii) TITLE OF THE INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS
 - (iii) NUMBER OF SEQUENCES: 9
 - (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Incyte Pharmaceuticals, Inc.
 - (B) STREET: 3174 Porter Drive
 - (C) CITY: Palo Alto
 - (D) STATE: CA
 - (E) COUNTRY: U.S.
 - (F) ZIP: 94304
 - (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Diskette
 - (B) COMPUTER: IBM Compatible
 - (C) OPERATING SYSTEM: DOS
 - (D) SOFTWARE: FastSEQ Version 1.5
 - (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: To Be Assigned
 - (B) FILING DATE: Filed Herewith
 - (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Billings, Lucy J.
 - (B) REGISTRATION NUMBER: 36,749
 - (C) REFERENCE/DOCKET NUMBER: PF-0114 US
 - (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 415-855-0555
 - (B) TELEFAX: 415-845-4166
- (2) INFORMATION FOR SEQ ID NO:1:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 199 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: peptide
 - (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY:
 - (B) CLONE: Consensus

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

```

Met Asp Gly Gln Lys Lys Asn Trp Lys Asp Lys Val Val Asp Leu Leu
1      5      10      15
Tyr Trp Arg Asp Ile Lys Lys Thr Gly Val Val Phe Gly Ala Ser Leu
20     25     30
Phe Leu Leu Leu Ser Leu Thr Val Phe Ser Ile Val Ser Val Thr Ala
35     40     45
Tyr Ile Ala Leu Ala Leu Leu Ser Val Thr Ile Ser Phe Arg Ile Tyr
50     55     60
Lys Gly Val Ile Gln Ala Ile Gln Lys Ser Asp Glu Gly His Pro Phe
65     70     75     80
Arg Ala Tyr Leu Glu Ser Glu Val Ala Ile Ser Glu Glu Leu Val Gln
85     90     95
Lys Tyr Ser Asn Ser Ala Leu Gly His Val Asn Cys Thr Ile Lys Glu
100    105    110
Leu Arg Arg Leu Phe Leu Val Asp Asp Leu Val Asp Ser Leu Lys Phe
115    120    125
Ala Val Leu Met Trp Val Phe Thr Tyr Val Gly Ala Leu Phe Asn Gly
130    135    140
Leu Thr Leu Leu Ile Leu Ala Leu Ile Ser Leu Phe Ser Val Pro Val
145    150    155    160
Ile Tyr Glu Arg His Gln Ala Gln Ile Asp His Tyr Leu Gly Leu Ala
165    170    175
Asn Lys Asn Val Lys Asp Ala Met Ala Lys Ile Gln Ala Lys Ile Pro
180    185    190
Gly Leu Lys Arg Lys Ala Glu
195

```

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 799 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY:
- (B) CLONE: Consensus

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

```

GGTTTGTGCA GTTACAGCTT TTCTNITGGT ATGCATAATT AATANTTGGA GCTGCAAAGA      60
GATCGTGACA AGAGATGGAC GGTCAGAAGA AAAATTGGAA GGACAAGGTT GTTGACCTCC      120
TGTACTGGAG AGACATTAAG AAGACTGGAG TGGTGTITGG TGCCAGCCTTA TTCCTGCTGC      180
TTTCATTGAC AGTATTCAGC ATTGTGAGCG TAACAGCCTA CATTCGCTTG GCCCTGCTCT      240
CTGTGACCAT CAGCTTTAGG ATATACAAGG GTGTGATCCA AGCTATCCAG AAATCAGATG      300
AAGGCCACCC ATTCAGGGCA TATCTGGAAT CTGAAGTTGC TATATCTGAG GAGTTGGTTC      360
AGAAGTACAG TAATTC7GCT CTTGGTCATG TGAAGTGCAC GATAAAGGAA CTCAGGCGCC      420
TCTTCTTAGT TGATGATTTA GTTGATTCTC TGAAGTTTGC AGTGTTCATG TGGGTATTTA      480
CCTAATGTTG TGCCATTGTT AATGGTCTGA CACTACTGAT TTTGGCTCTC ATTTCACTCT      540
TCAGTGTTCG TGTTATTATG GAACGGCATC AGGCACAGAT AGATCATTAT CTAGGACTTG      600
CAAAAGAGAA TGTTAAAGAT GCTATGGCTA AAATCCAAGC AAAAATCCCT GGATTGAAGC      660
GCAAAGCTGA ATGAAACGCG CCAAAATAAT TAGTAGGAGT TCATCTTTAA AGGGGATATT      720

```

CATTGATTA TACGGGGGAG GGTGAGGGAA GAACGACCTT GACGTTGCAG TGCAGTTTCA
CAGATCGTTG TTAGATCTT

780
799

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 241 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: THP1NOB01
- (B) CLONE: 31870

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met	Ala	Glu	Arg	Xaa	Ala	Ala	Thr	Gln	Ser	His	Ser	Ile	Ser	Ser	Ser	15
1				5				10								
Ser	Phe	Gly	Ala	Glu	Pro	Ser	Ala	Pro	Gly	Gly	Gly	Gly	Ser	Pro	Gly	30
			20					25								
Ala	Cys	Pro	Ala	Leu	Gly	Thr	Lys	Ser	Cys	Ser	Ser	Ser	Cys	Ala	Val	45
			35					40								
His	Asp	Leu	Ile	Xaa	Trp	Arg	Asp	Val	Lys	Lys	Thr	Gly	Phe	Val	Phe	60
			50					55								
Gly	Thr	Thr	Leu	Ile	Met	Leu	Leu	Ser	Leu	Ala	Ala	Phe	Ser	Val	Ile	75
			65					70								
Ser	Val	Val	Ser	Tyr	Leu	Ile	Leu	Ala	Leu	Leu	Ser	Val	Thr	Ile	Ser	90
				85												
Phe	Arg	Ile	Tyr	Lys	Ser	Val	Ile	Gln	Ala	Val	Gln	Lys	Ser	Glu	Glu	105
				100												
Gly	His	Pro	Phe	Lys	Ala	Tyr	Leu	Asp	Val	Asp	Ile	Thr	Leu	Ser	Ser	120
				115												
Glu	Ala	Phe	His	Asn	Tyr	Met	Asn	Ala	Ala	Met	Val	His	Ile	Asn	Arg	135
				130												
Ala	Leu	Lys	Leu	Ile	Ile	Arg	Leu	Phe	Leu	Val	Glu	Asp	Leu	Val	Asp	150
				145												
Ser	Leu	Lys	Leu	Ala	Val	Phe	Met	Trp	Leu	Met	Thr	Tyr	Val	Gly	Ala	165
				160												
Val	Phe	Asn	Gly	Ile	Thr	Leu	Leu	Ile	Leu	Ala	Glu	Leu	Leu	Ile	Xaa	180
				175												
Ser	Val	Pro	Ile	Val	Tyr	Xaa	Lys	Tyr	Lys	Val	Pro	Ser	Lys	Thr	Pro	195
				190												
Trp	Asn	Arg	Gln	Lys	Lys	Gly	Arg	Ile	Ser	Thr	Trp	Lys	Pro	Glu	Met	210
				205												
Gln	Gln	Leu	Leu	Lys	His	His	Leu	Ile	Val	Ile	Thr	Ser	Leu	Leu	Val	225
				220												
Leu					230					235						240

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1095 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

PF-0114 US

- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (vii) IMMEDIATE SOURCE:
- (A) LIBRARY: THF1NOB01
- (B) CLONE: 31870
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

```
ACACNAGCGN NTCGNGCTCC CGAACCTCTA GCTGCGACTC GGANTGAGTC AGTCAGTCTG 60
TCGGAGTCTG TCCTCGGAGC AGGCGGAGTA AAGGGACTTG AGCGAGCCAG TTGCCGGATT 120
ATTCTATTTT CCCTCCCTCT CTCCCGCCCC GTATCTCTTT TCATTTTNNNT NCCACCCCTTG 180
CTCGCGTANC ATGGCGGAGC GTNCGGCGGC CACTCAGTCC CATTCCATCT CCTCGTCGTC 240
CTTCGGAGCC GAGCCGTCCG CGCCCGGCGG CGCGGGGAGC CCAGGAGCCT GCCCCGCCCT 300
GGGGACGAAG AGCTGCAGCT CCTCCTGTGC GGTGACGAT CTGATTTTMT GGAGAGATGT 360
GAAGAAGACT GGGTTGTCTT TTGGCACCAC GCTGATCATG CTGCTTTCCC TGGCAGCTTT 420
CAGTGTCACT AGTGTGGTTT CTTACCTCAT CTGGCTCTT CTCTCTGTCA CCATCAGCTT 480
CAGGATCTAC AAGTCCGTC TCCAAGCTGT ACAGAAGTCA GAAGAAGGCC ATCCATTCAA 540
AGCCTACCTG GACGTAGACA TTACTCTGTC CTCAGAAGCT TTCCATAATT ACATGAATGC 600
TGCCATGGTG CACATCAACA GGGCCCTGAA ACTCATTATT CGTCTCTTTC TGGTAGAAGA 660
TCTGTTGAC TCCTTGAAGC TGGCTGTCTT CATGTGGCTG ATGACCTATG TTGGTGTCTG 720
TTTTAAGCGA ATCACCCTTC TAATTCTTGC TGAAGTGCCT ATTTTNAGTG TCCCGATTGT 780
NTATNAGAAG TACAAGGTTT CAAGCAAAAC TCCTTGAAT CGCCAAAAAA AAGGCAGAA 840
AAGTACATGG AAACCAAGAA TGCAACAGTT ACTAAAAAC CATTTAATAG TTATAACGTC 900
GTTACTTGTA CTATGAAGAA AAATACTCAG TGTCAGCTTG AGCCTGCATT CCAAGCTTTT 960
TTTTTAATTT GGTGGTTTTC TCCCATCCTT TCCCTTTAAC CCTCAGTNTC AAGCACAAAN 1020
TTNATGGAC TGATAANNGA TCTATNTTAG ANCTCAGAA ANGANAGNTT CANNTGCATA 1080
GGNTAAGGNA NTACC 1095
```

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 776 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (vii) IMMEDIATE SOURCE:
- (A) LIBRARY: GenBank
- (B) CLONE: 307307
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

```
Met Ala Ala Pro Gly Asp Pro Gln Asp Glu Leu Leu Pro Leu Ala Gly
1      5      10      15
Pro Gly Ser Gln Trp Leu Arg His Arg Gly Glu Gly Glu Asn Glu Ala
20     25     30
Val Thr Pro Lys Gly Ala Thr Pro Ala Pro Gln Ala Gly Glu Pro Ser
35     40     45
Pro Gly Leu Gly Ala Arg Ala Arg Glu Ala Ala Ser Arg Glu Ala Gly
50     55     60
Ser Gly Pro Ala Arg Gln Ser Pro Val Ala Met Glu Thr Ala Ser Thr
65     70     75     80
```

PF-0114 US

Gly	Val	Ala	Gly	Val	Ser	Ser	Ala	Met	Asp	His	Thr	Phe	Ser	Thr	Thr	
			85						90					95		
Ser	Lys	Asp	Gly	Glu	Gly	Ser	Cys	Tyr	Thr	Ser	Leu	Ile	Ser	Asp	Ile	
			100					105					110			
Cys	Tyr	Pro	Pro	Gln	Glu	Asp	Ser	Thr	Tyr	Phe	Thr	Gly	Ile	Leu	Gln	
			115					120				125				
Lys	Glu	Asn	Gly	His	Val	Thr	Ile	Ser	Glu	Ser	Pro	Glu	Glu	Leu	Gly	
			130					135				140				
Thr	Pro	Gly	Pro	Ser	Leu	Pro	Asp	Val	Pro	Gly	Ile	Glu	Ser	Arg	Gly	
			145					150			155				160	
Leu	Phe	Ser	Ser	Asp	Ser	Gly	Ile	Glu	Met	Thr	Pro	Ala	Glu	Ser	Thr	
				165					170					175		
Glu	Val	Asn	Lys	Ile	Leu	Ala	Asp	Pro	Leu	Asp	Gln	Met	Lys	Ala	Glu	
			180					185					190			
Ala	Tyr	Lys	Tyr	Ile	Asp	Ile	Thr	Arg	Pro	Glu	Glu	Val	Lys	His	Gln	
			195					200				205				
Glu	Gln	His	His	Pro	Glu	Leu	Glu	Asp	Lys	Asp	Leu	Asp	Phe	Lys	Asn	
			210					215				220				
Lys	Asp	Thr	Asp	Ile	Ser	Ile	Lys	Pro	Glu	Gly	Val	Arg	Glu	Pro	Asp	
			225					230			235				240	
Lys	Pro	Ala	Pro	Val	Glu	Gly	Lys	Ile	Ile	Lys	Asp	His	Leu	Leu	Glu	
				245					250				255			
Glu	Ser	Thr	Phe	Ala	Pro	Tyr	Ile	Asp	Asp	Leu	Ser	Glu	Glu	Gln	Arg	
			260					265					270			
Arg	Ala	Pro	Gln	Ile	Thr	Thr	Pro	Val	Lys	Ile	Thr	Leu	Thr	Glu	Ile	
			275					280				285				
Glu	Pro	Ser	Val	Glu	Thr	Thr	Gln	Glu	Lys	Thr	Pro	Glu	Lys	Gln		
			290					295			300					
Asp	Ile	Cys	Leu	Lys	Pro	Ser	Pro	Asp	Thr	Val	Pro	Thr	Val	Thr	Val	
			305					310			315				320	
Ser	Glu	Pro	Glu	Asp	Asp	Ser	Pro	Gly	Ser	Ile	Thr	Pro	Pro	Ser	Ser	
				325					330					335		
Gly	Thr	Glu	Pro	Ser	Ala	Ala	Glu	Ser	Gln	Gly	Lys	Gly	Ser	Ile	Ser	
			340					345					350			
Glu	Asp	Glu	Leu	Ile	Thr	Ala	Ile	Lys	Glu	Ala	Lys	Gly	Leu	Ser	Tyr	
			355					360				365				
Glu	Thr	Ala	Glu	Asn	Pro	Arg	Pro	Val	Gly	Gln	Leu	Ala	Asp	Arg	Pro	
			370					375				380				
Glu	Val	Lys	Ala	Arg	Ser	Gly	Pro	Pro	Thr	Ile	Pro	Ser	Pro	Leu	Asp	
			385					390			395				400	
His	Glu	Ala	Ser	Ser	Ala	Glu	Ser	Gly	Asp	Ser	Glu	Ile	Glu	Leu	Val	
			405						410					415		
Ser	Glu	Asp	Pro	Met	Ala	Ala	Glu	Asp	Ala	Leu	Pro	Ser	Gly	Tyr	Val	
			420					425					430			
Ser	Phe	Gly	His	Val	Gly	Gly	Pro	Pro	Pro	Ser	Pro	Ala	Ser	Pro	Ser	
			435					440				445				
Ile	Gln	Tyr	Ser	Ile	Leu	Arg	Glu	Glu	Arg	Glu	Ala	Glu	Leu	Asp	Ser	
			450					455			460					
Glu	Leu	Ile	Ile	Glu	Ser	Cys	Asp	Ala	Ser	Ser	Ala	Ser	Glu	Glu	Ser	
			465					470			475				480	
Pro	Lys	Arg	Glu	Gln	Asp	Ser	Pro	Pro	Met	Lys	Pro	Ser	Ala	Leu	Asp	
				485					490				495			
Ala	Ile	Arg	Glu	Glu	Thr	Gly	Val	Arg	Ala	Glu	Glu	Arg	Ala	Pro	Ser	
			500					505					510			
Arg	Arg	Gly	Leu	Ala	Glu	Pro	Gly	Ser	Phe	Leu	Asp	Tyr	Pro	Ser	Thr	
			515					520				525				

PF-0114 US

```

Glu Pro Gln Pro Gly Pro Glu Leu Pro Pro Gly Asp Gly Ala Leu Glu
530 535 540
Pro Glu Thr Pro Met Leu Pro Arg Lys Pro Glu Glu Asp Ser Ser Ser
545 550 560
Asn Gln Ser Pro Ala Ala Thr Lys Gly Pro Gly Pro Leu Gly Pro Gly
565 570 575
Ala Pro Pro Pro Leu Leu Phe Leu Asn Lys Gln Lys Ala Ile Asp Leu
580 585 590
Leu Tyr Trp Arg Asp Ile Lys Gln Thr Gly Ile Val Phe Gly Ser Phe
595 600 605
Leu Leu Leu Leu Phe Ser Leu Thr Gln Phe Ser Val Val Ser Val Val
610 615 620
Ala Tyr Leu Ala Leu Ala Ala Leu Ser Ala Thr Ile Ser Phe Arg Ile
625 630 635 640
Tyr Lys Ser Val Leu Gln Ala Val Gln Lys Thr Asp Glu Gly His Pro
645 650 655
Phe Lys Ala Tyr Leu Glu Leu Glu Ile Thr Leu Ser Gln Glu Gln Ile
660 665 670
Gln Lys Tyr Thr Asp Cys Leu Gln Phe Tyr Val Asn Ser Thr Leu Lys
675 680 685
Glu Leu Arg Arg Leu Phe Leu Val Gln Asp Leu Val Asp Ser Leu Lys
690 695 700
Phe Ala Val Leu Met Trp Leu Leu Thr Tyr Val Gly Ala Leu Phe Asn
705 710 715 720
Gly Leu Thr Leu Leu Met Ala Val Val Ser Met Phe Thr Leu Pro
725 730 735
Val Val Tyr Val Lys His Gln Ala Gln Ile Asp Gln Tyr Leu Gly Leu
740 745 750
Val Arg Thr His Ile Asn Ala Val Val Ala Lys Ile Gln Ala Lys Ile
755 760 765
Pro Gly Ala Lys Arg His Ala Glu
770 775

```

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 356 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: GenBank
- (B) CLONE: 307309

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

```

Met Ala Ala Glu Asp Ala Leu Pro Ser Gly Tyr Val Ser Phe Gly His
1 5 10 15
Val Gly Gly Pro Pro Pro Ser Pro Ala Ser Pro Ser Ile Gln Tyr Ser
20 25 30
Ile Leu Arg Glu Glu Arg Glu Ala Glu Leu Asp Ser Glu Leu Ile Ile
35 40 45
Glu Ser Cys Asp Ala Ser Ser Ala Ser Glu Glu Ser Pro Lys Arg Glu
50 55 60

```

PF-0114 US

```

Gln Asp Ser Pro Pro Met Lys Pro Ser Ala Leu Asp Ala Ile Arg Glu
65      70      75
Glu Thr Gly Val Arg Ala Glu Glu Arg Ala Pro Ser Arg Arg Gly Leu
      85      90      95
Ala Glu Pro Gly Ser Phe Leu Asp Tyr Pro Ser Thr Glu Pro Gln Pro
100      105      110
Gly Pro Glu Leu Pro Pro Gly Asp Gly Ala Leu Glu Pro Glu Thr Pro
115      120      125
Met Leu Pro Arg Lys Pro Glu Glu Asp Ser Ser Ser Asn Gln Ser Pro
130      135      140
Ala Ala Thr Lys Gly Pro Gly Pro Leu Gly Pro Gly Ala Pro Pro Pro
145      150      155      160
Leu Leu Phe Leu Asn Lys Gln Lys Ala Ile Asp Leu Leu Tyr Trp Arg
165      170      175
Asp Ile Lys Gln Thr Gly Ile Val Phe Gly Ser Phe Leu Leu Leu Leu
180      185      190
Phe Ser Leu Thr Gln Phe Ser Val Val Ser Val Val Ala Tyr Leu Ala
195      200      205
Leu Ala Ala Leu Ser Ala Thr Ile Ser Phe Arg Ile Tyr Lys Ser Val
210      215      220
Leu Gln Ala Val Gln Lys Thr Asp Glu Gly His Pro Phe Lys Ala Tyr
225      230      235      240
Leu Glu Leu Glu Ile Thr Leu Ser Gln Glu Gln Ile Gln Lys Tyr Thr
245      250      255
Asp Cys Leu Gln Phe Tyr Val Asn Ser Thr Leu Lys Glu Leu Arg Arg
260      265      270
Leu Phe Leu Val Gln Asp Leu Val Asp Ser Leu Lys Phe Ala Val Leu
275      280      285
Met Trp Leu Leu Thr Tyr Val Gly Ala Leu Phe Asn Gly Leu Thr Leu
290      295      300
Leu Leu Met Ala Val Val Ser Met Phe Thr Leu Pro Val Val Tyr Val
305      310      315      320
Lys His Gln Ala Gln Ile Asp Gln Tyr Leu Gly Leu Val Arg Thr His
325      330      335
Ile Asn Ala Val Val Ala Lys Ile Gln Ala Lys Ile Pro Gly Ala Lys
340      345      350
Arg His Ala Glu
355

```

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 208 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: GenBank
- (B) CLONE: 307311

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

```

Met Gln Ala Thr Ala Asp Ser Thr Lys Met Asp Cys Val Trp Ser Asn
1      5      10      15

```

PF-0114 US

```

Trp Lys Ser  Gln Ala Ile Asp Leu Leu Tyr Trp Arg Asp  Ile Lys Gln
      20      25      30
Thr Gly Ile Val Phe Gly Ser  Phe Leu Leu Leu Phe Ser  Leu Thr
      35      40      45
Gln Phe Ser Val Val Ser Val Val Ala Tyr Leu Ala Leu Ala Leu
      50      55      60
Ser Ala Thr Ile Ser  Phe Arg Ile Tyr Lys Ser Val Leu Gln Ala Val
      65      70      75      80
Gln Lys Thr Asp Glu Gly His Pro Phe Lys Ala Tyr Leu Glu Leu Glu
      85      90      95
Ile Thr Leu Ser  Gln Glu Gln Ile Gln Lys Tyr Thr Asp Cys Leu Gln
      100      105      110
Phe Tyr Val Asn Ser Thr Leu Lys Glu Leu Arg Arg Leu Phe Leu Val
      115      120      125
Gln Asp Leu Val Asp Ser Leu Lys Phe Ala Val Leu Met Trp Leu Leu
      130      135      140
Thr Tyr Val Gly Ala Leu Phe Asn Gly Leu Thr Leu Leu Leu Met Ala
      145      150      155      160
Val Val Ser Met Phe Thr Leu Pro Val Val Tyr Val Lys His Gln Ala
      165      170      175
Gln Ile Asp Gln Tyr Leu Gly Leu Val Arg Thr His Ile Asn Ala Val
      180      185      190
Val Ala Lys Ile Gln Ala Lys Ile Pro Gly Ala Lys Arg His Ala Glu
      195      200      205

```

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 267 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: GenBank
- (B) CLONE: 281046

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

```

Met Asp Cys Val Trp Ser Asn Trp Lys Ser Gln Ala Ile Asp Leu Leu
  1      5      10      15
Tyr Trp Arg Asp Ile Lys Gln Thr Gly Ile Val Phe Gly Ser Phe Leu
  20      25      30
Leu Leu Leu Phe Ser Leu Thr Gln Phe Ser Val Val Ser Val Val Ala
  35      40      45
Tyr Leu Ala Leu Ala Ala Leu Ser Ala Thr Ile Ser Phe Arg Ile Tyr
  50      55      60
Lys Ser Val Leu Gln Ala Val Gln Lys Thr Asp Glu Gly His Pro Phe
  65      70      75      80
Lys Ala Tyr Leu Glu Leu Glu Ile Thr Leu Ser Gln Glu Gln Ile Gln
  85      90      95
Lys Tyr Thr Asp Cys Leu Gln Leu Tyr Val Asn Ser Thr Leu Lys Glu
  100      105      110
Leu Arg Arg Leu Phe Leu Val Gln Asp Leu Val Asp Ser Leu Lys Phe
  115      120      125

```


PF-0114 US

```

Ala Val Leu Met Trp Leu Leu Thr Tyr Val Gly Ala Leu Phe Asn Gly
130                      135                      140
Leu Thr Leu Leu Leu Met Ala Val Val Ser Met Phe Thr Leu Pro Val
145                      150                      155                      160
Val Tyr Val Lys His Gln Ala Gln Val Asp Gln Tyr Leu Gly Leu Val
165                      170                      175
Arg Thr His Ile Asn Thr Val Val Ala Lys Ile Gln Ala Lys Ile Pro
180                      185                      190
Gly Ala Arg Gly Met Leu Ser Arg Trp Leu Pro Gln Glu Lys Pro Asp
195                      200                      205
Met Asn Gly Gly Val Trp Ser Gly Asn Ser Ser Leu Leu Pro Arg Tyr
210                      215                      220
Cys Glu Leu Ile Val Ser Leu Pro Gln Tyr His Asn Leu Arg Gly Lys
225                      230                      235                      240
Leu Arg Asp Arg Cys Phe Gln Ser Phe Pro Val Leu Leu Gly Tyr Leu
245                      250                      255
Ser Pro Pro Arg Pro Leu Ser Ser Thr Lys Val
260                      265

```

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 261 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: SPLNFET01
- (B) CLONE: 28742

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

```

CCTATNCNG  CTGCTTTCAT  TGACAGTATT  CAGCATTGTG  AGCGTAACAG  CCTACATTGC  60
CTTNGCCCTG  CNCTCTGTGA  CCATCAGCTN  TAGGCTATAC  AAGGGTGTGA  TCCAAGCTAT  120
CCAGAAATCA  GATGAAGGNC  ACCCATTCAG  GGCATATCTG  GANTCTGAAG  TTGCTATATC  180
TGAGGAGTTG  NTTCAGAAGT  ACACGTAAT  NNTGNNCNTG  GTCAATGTGA  NCTCCACGNC  240
TAANGANCT  CAGGTGCCTA  T

```